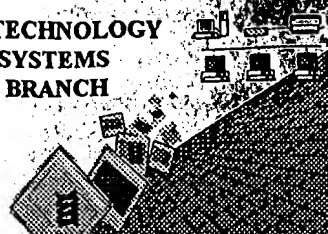


K. Davis

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BIOTECHNOLOGY
SYSTEMS
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20/358
2/21/02

**RAW SEQUENCE LISTING
ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

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FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

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Revised 01/29/2002



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/487,558A

DATE: 02/14/2002

TIME: 14:23:29

Input Set : D:\MIC-001USptn.ST25.txt

Output Set: N:\CRF3\02142002\I487558A.raw

Does Not Comply
Corrected Diskette Needed

4 <110> APPLICANT: Busby, Robert
5 Cali, Brian
6 Hecht, Peter
7 Holtzman, Doug
8 Madden, Kevin
9 Maxon, Mary
10 Milne, Todd
11 Norman, Thea
12 Royer, John
13 Salama, Sofie
14 Sherman, Amir
15 Silva, Jeff
16 Summers, Eric
18 <120> TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in
Fungi
20 <130> FILE REFERENCE: 109272.130
W--> 22 ~~<130> FILE REFERENCE: 109272-130~~ *delete - already shown above*
24 <140> CURRENT APPLICATION NUMBER: 09/487,558A
25 <141> CURRENT FILING DATE: 2000-01-19
27 <150> PRIOR APPLICATION NUMBER: US 60/487,558
28 <151> PRIOR FILING DATE: 1999-10-20
E--> 30 <160> NUMBER OF SEQ ID NOS: ~~440~~ 446 (p. 2)
32 <170> SOFTWARE: PatentIn version 3.0

ERRORED SEQUENCES

<210> 446 *last sequence in file*
<211> 24
<212> DNA
<213> Saccaromyces cerevesiae

<400> 446
gttaagcagg aattaccgac acca

24

FYI Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

~~VERIFICATION SUMMARY~~

~~DATE: 02/14/2002~~

PATENT APPLICATION: US/09/487,558A

TIME: 14:23:38

Input Set : D:\MIC-001USptn.ST25.txt

Output Set: N:\CRF3\02142002\I487558A.raw

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L:98 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:99 M:283 W: Missing Blank Line separator, <220> field identifier
L:112 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:113 M:283 W: Missing Blank Line separator, <220> field identifier
L:126 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:127 M:283 W: Missing Blank Line separator, <220> field identifier
L:140 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:141 M:283 W: Missing Blank Line separator, <220> field identifier
L:30 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (440) Counted (446)